

10 20 30 40 50 60 70

GAT CACTGGG ACCAGGCCGT GATCTCTATG CCCGAGTTC AACCTCAAC TGTCCCCA AGGCACCTGG

80 90 100 110 120 130 140

GACGTCCTGG ACAGACCGAG TCCCGGGAAAG CCCCAGCACT GCCGCTGCCA CACTGCCCTG AGCCCCAAATG

150 160 171 180 189 198

GGGGAGTGAG AGGCCATAGC TGTCTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG
MET Gly Leu Ser Thr Val Pro Asp Leu Leu

207 216 225 234 243 252

CTG CCG CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT
Leu Pro Leu Val Leu Glu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile

261 270 279 288 297 306

GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC CAA
Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln

315 324 333 342 351 360

GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC AAG TGC CAC AAA
Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys

369 378 387 396 405 414

GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gln Asp Thr Asp Cys Arg

423 432 441 450 459 468

GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu

477 486 495 504 513 522

AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA
Ser Cys Ser Lys Cys Arg Lys Glu MET Gly Gln Val Glu Ile Ser Ser Cys Thr

531 540 549 558 567 576

GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG
Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp

585 594 603 612 621 630

AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG
Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gln Gly Thr Val

639 648 657 666 675 684

CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC
His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe

Fig. 21

693 702 711 720 729 738

TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG
Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu

747 756 765 774 783 792

TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG AAT GTT AAG GCG ACT GAG GAC TCA
Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser

801 810 819 828 837 846

GGC ACC ACA G TG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA TCC
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser

855 864 873 882 891 900

CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG TCC AAG CTC TAC
Leu Leu Phe Ile Gly Leu MET Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr

909 918 927 936 945 954

TCC ATT G TT TGT GGG AAA TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA GGA ACT
Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr

963 972 981 990 999 1008

ACT ACT AAG CCC CTG GCC CCA AAC CCA AGC TTC AGT CCC ACT CCA G GC TTC ACC
Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr

1017 1026 1035 1044 1053 1062

CCC ACC CTG G GC TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC
Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr

1071 1080 1089 1098 1107 1116

TAT ACC CCC GGT GAC T GT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA
Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro

1125 1134 1143 1152 1161 1170

CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC CCC ATC
Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile

1179 1188 1197 1206 1215 1224

CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC
Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp

1233 1242 1251 1260 1269 1278

ACT GAT GAC CCC GCG ACG CTG TAC GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg

1287 1296 1305 1314 1323 1332

TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG AGC GAC CAC GAG ATC GAT CGG CTG
Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu

FIG. 21

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1341 1350 1359 1368 1377 1386

GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC
Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser MET Leu Ala Thr

1395 1404 1413 1422 1431 1440

TGG AGG CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG CTG GGA CGC GTC
Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val

1449 1458 1467 1476 1485 1494

CTC CGC GAC ATG GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC
Leu Arg Asp MET Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys

1503 1512 1521 1530 1546 1556

GGC CCC GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGA GGCTGCGCCC CTGCGGGCAG
Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg

1566 1576 1586 1596 1606 1616 1626

CTCTAAGGAC CGTCCTGCGA GATGCCCTTC CAACCCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG

1636 1646 1656 1666 1676 1686 1696

CAAGCAGGAG CTAGCAGCCG CCTACTTGCT GCTAACCCCT CGATGTACAT AGCTTTCTC AGCTGCCTGC

1706 1716 1726 1736 1746 1756 1766

GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT GAGTGGGTGG

1776 1786 1796 1806 1816 1826 1836

TTTGCAGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTG GGTGTCCCTCA CCAGCAAGGC TGCTCGGGGG

1846 1856 1866 1876 1886 1896 1906

CCCCCTGGTTTC GTCCCTGAGC CTTTTCACA GTGCATAAGC AGTTTTTTTT GTTTTTGTAA TGTTTTGTAA

1916 1926 1936 1946 1956 1966 1976

TGTTTTTAAA TCAATCATGT TACACTAATA GAAACTTGGC ACTCCTGTGC CCTCTGCCTG GACAAGCACA

1986 1996 2006 2016 2026 2036 2046

TAGCAAGCTG AACTGTCTTA AGGCAGGGGC GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT

2056 2066 2076 2086

TTTGTACATA CACTAAAATT CTGAAGTTAA AGCTCAAAAA AA

FIG. 21